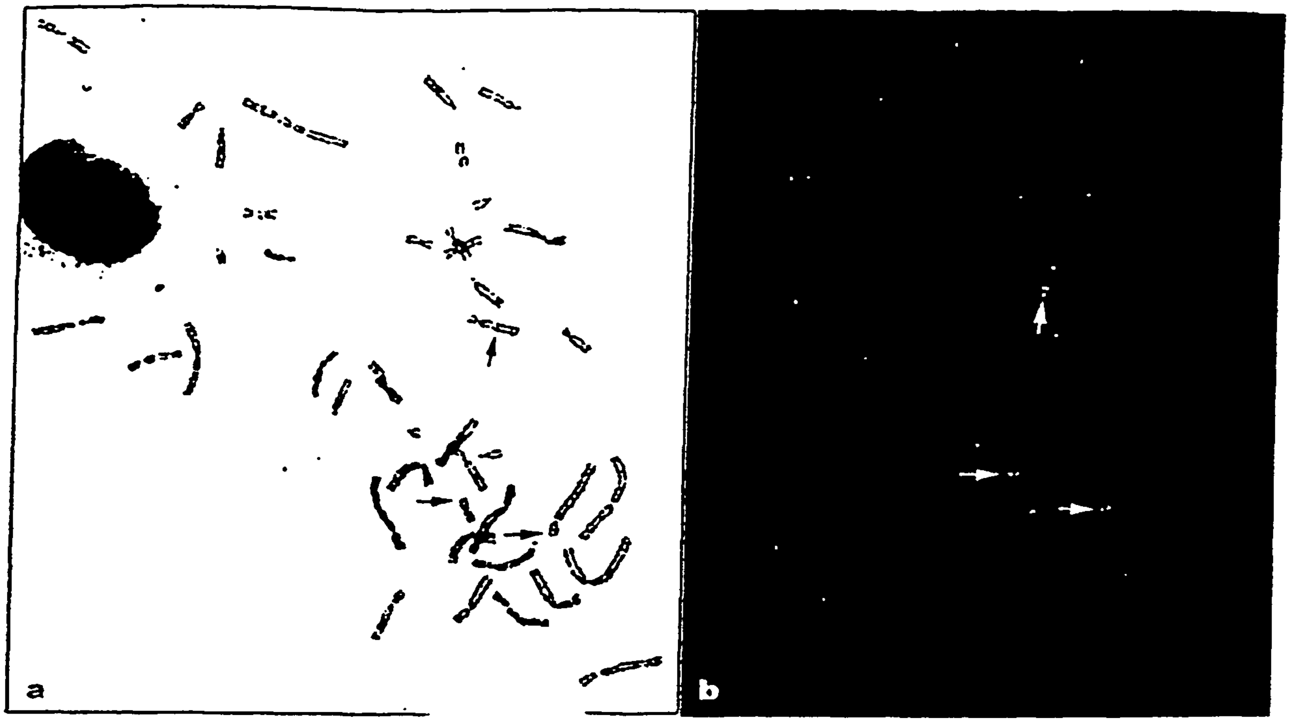
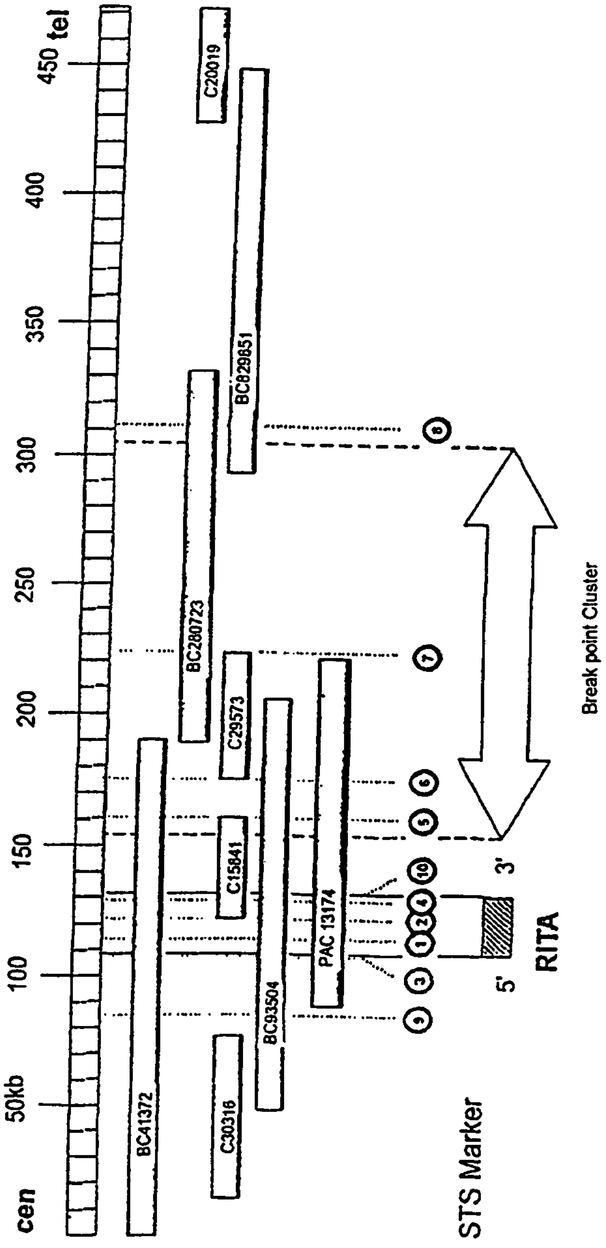


Fig. 1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BC280723
BC829851
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3
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10
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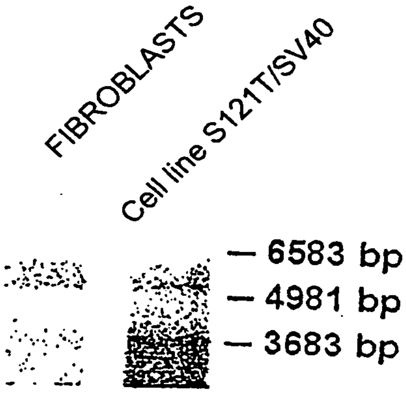
6
7
8
5'
3'
RITA
Break point Cluster

Fig. 2



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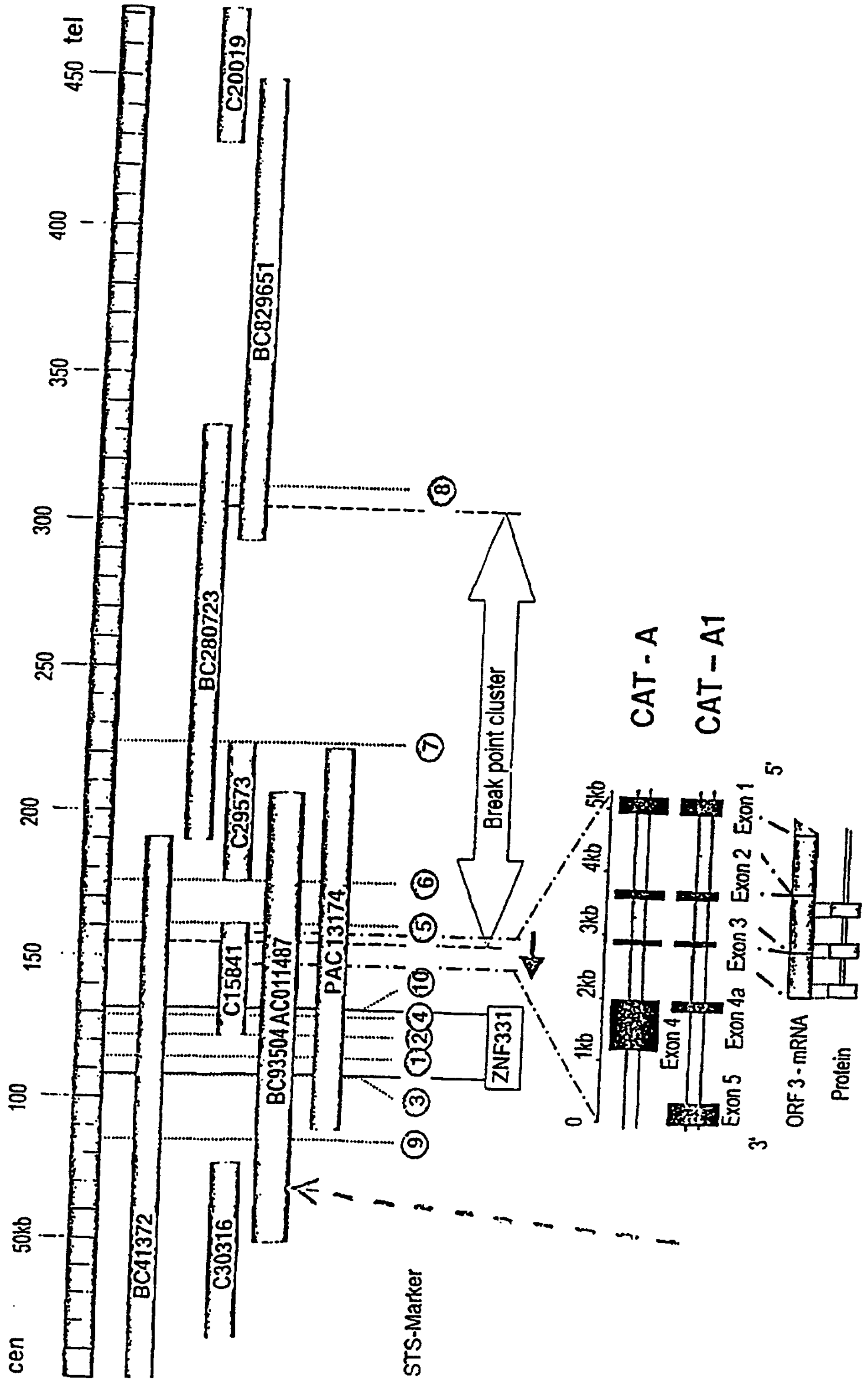
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PAC13174
BC280723
BC829651
C20019
STS-Marker
⑨
③
①
②
④
⑩
⑤
⑥
⑦
⑧
ZNF331
Break point cluster
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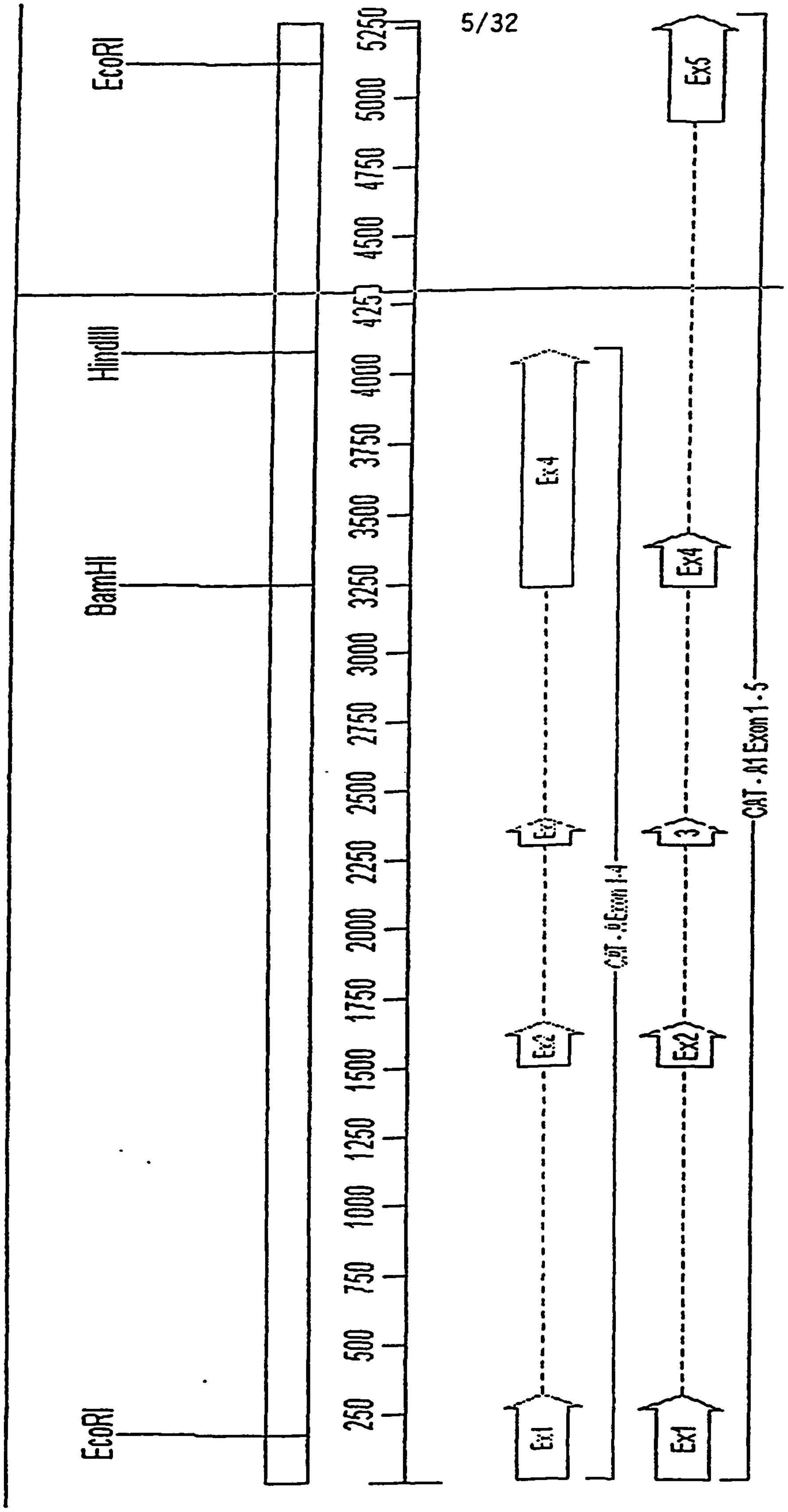
1kb
2kb
3kb
4kb
5kb
CAT - A
CAT - A1
Exon 5
Exon 4
Exon 4a
Exon 3
Exon 2
Exon 1
3'
5'
ORF 3 - mRNA
Protein

Fig. 4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Ex1
Ex2
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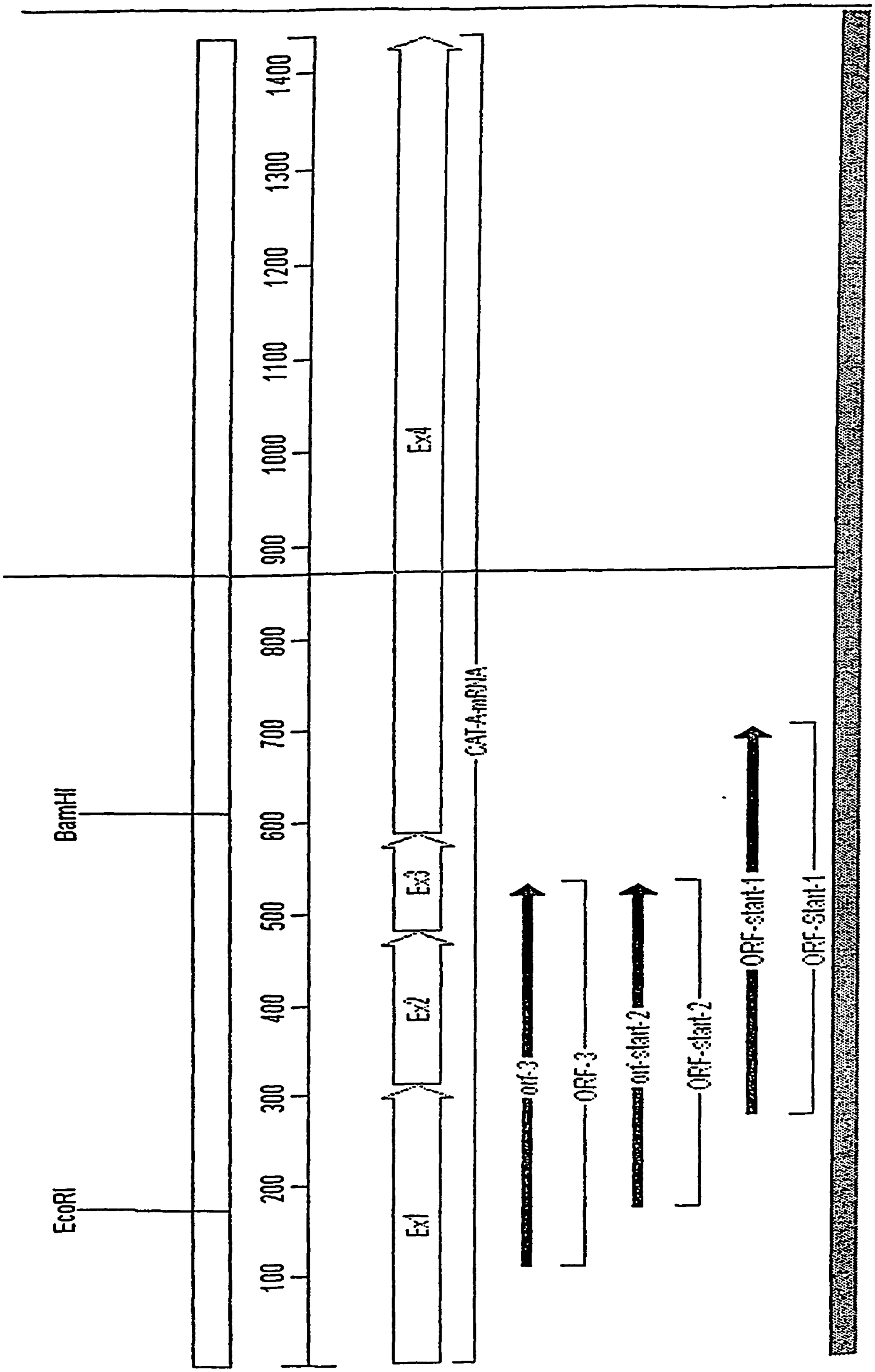
Ex4
Ex5
CAT - A1 Exon 1 - 5

Fig. 5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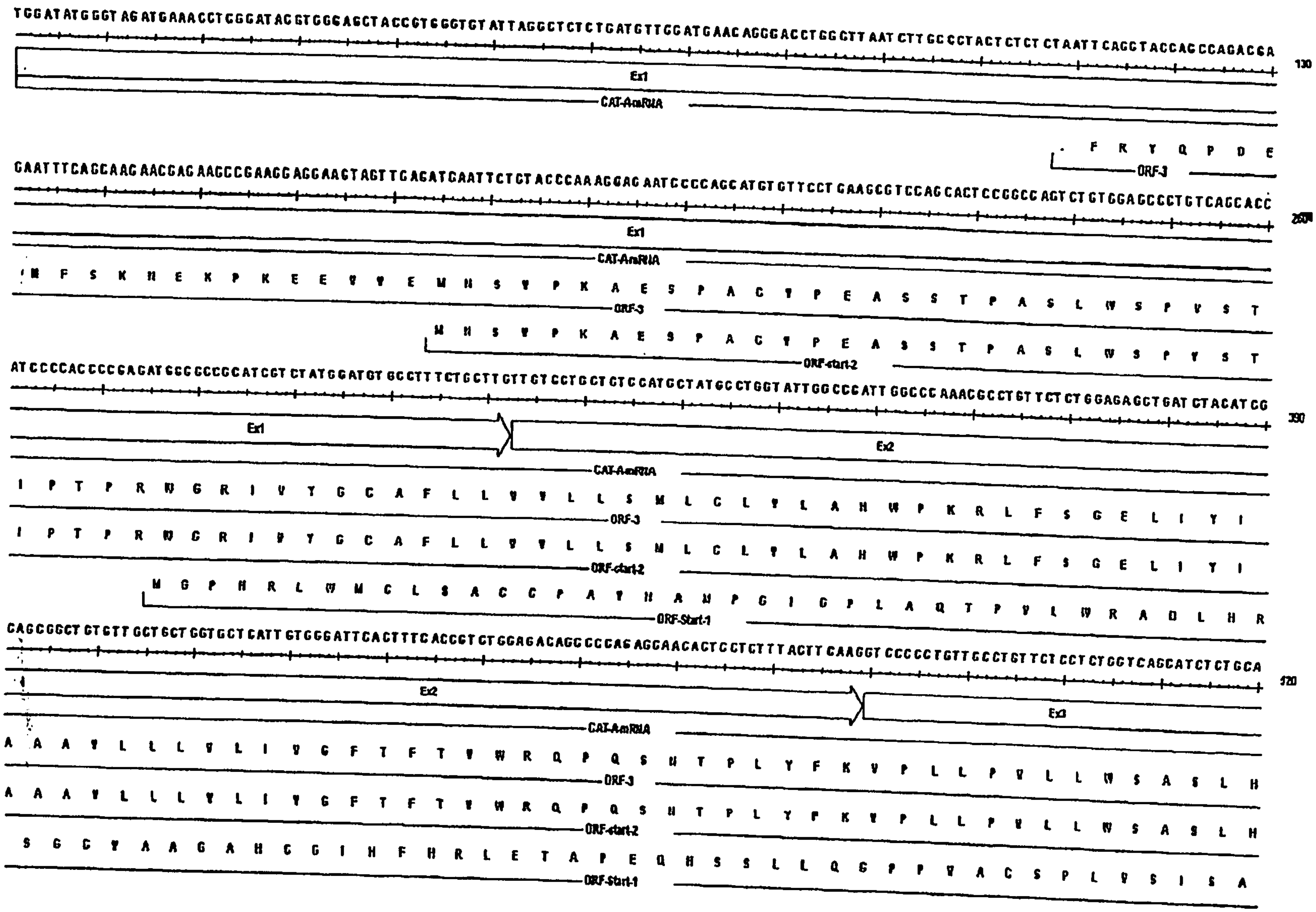
ORF-start-2
ORF-start-1
ORF-Start-1

Fig. 6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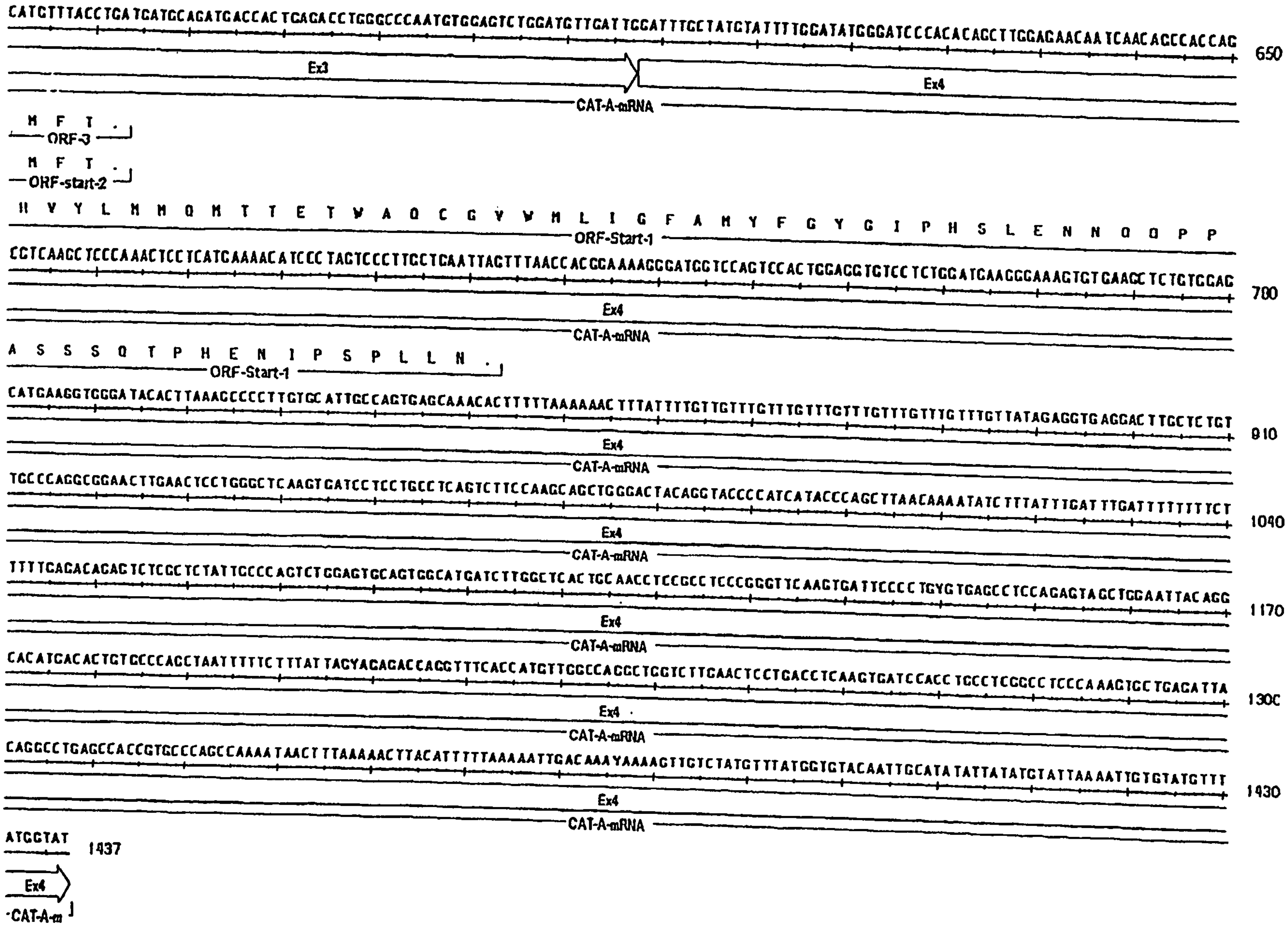
ORF-Start-1

Fig. 7 Part 1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Ex4
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M F T .
ORF-3
M F T .
ORF-start-2
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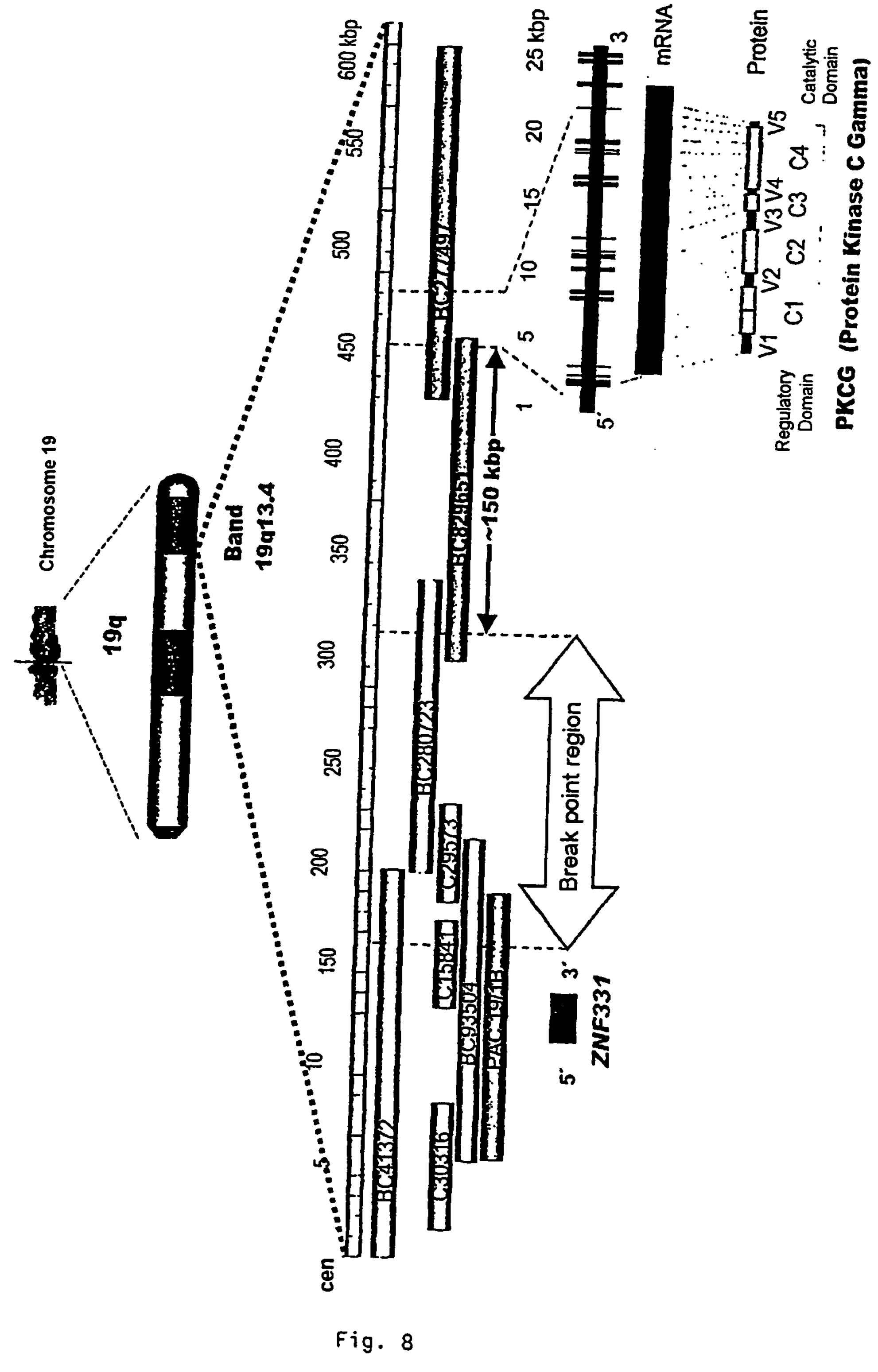
Fig. 7 Part 2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BC277497
~150 kbp
Break point region
5'
3'
ZNF331
1
5
10
15
20
25 kbp
5'
3
mRNA
Protein
V1
C1
V2
C2
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C3
V4
C4
V5
Regulatory
Domain
Catalytic
Domain
PKCG (Protein Kinase C Gamma)

Fig. 8

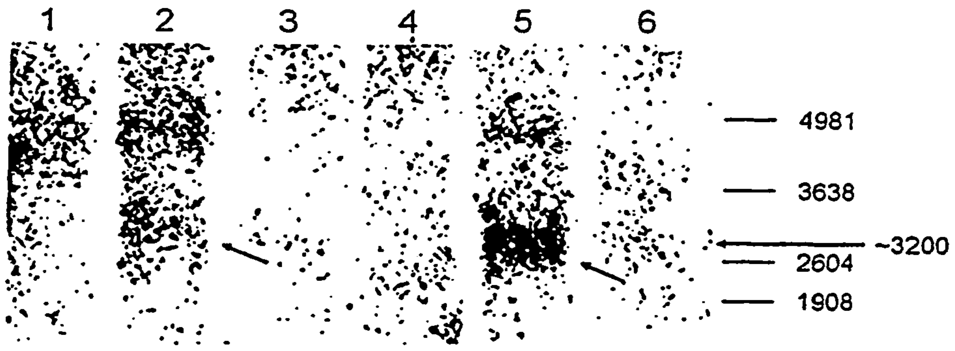
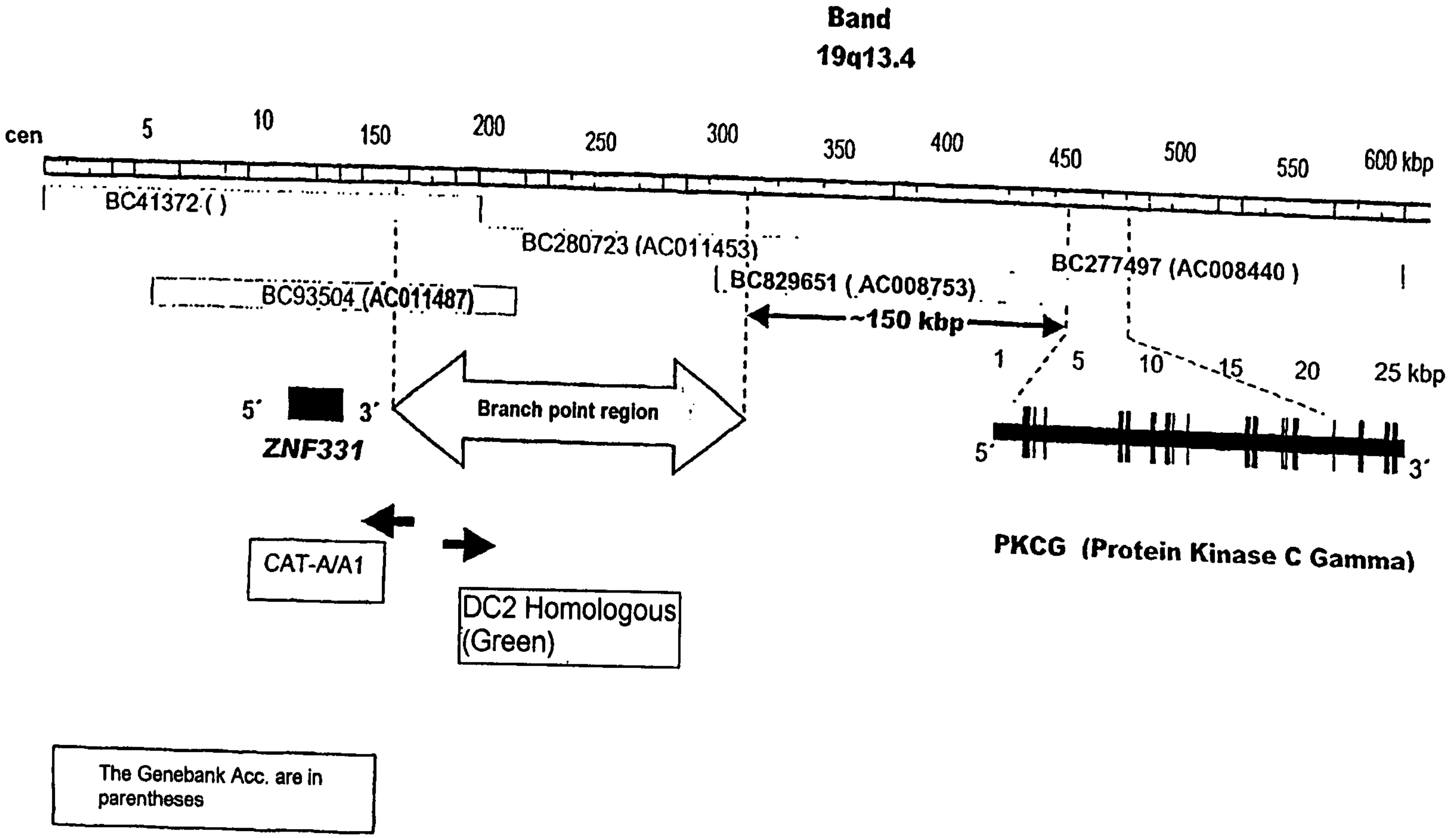


Fig. 9

Fig. 10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10
15
20
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5'
3'
ZNF331
Branch point region
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CAT-A/A1
DC2 Homologous
(Green)
The Genebank Acc. are in parentheses

Fig. 11

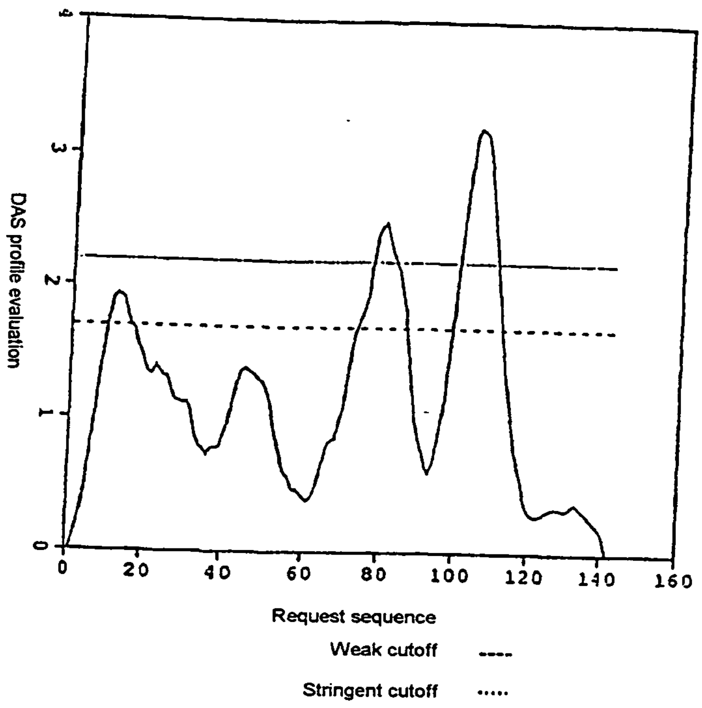
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Fig. 12

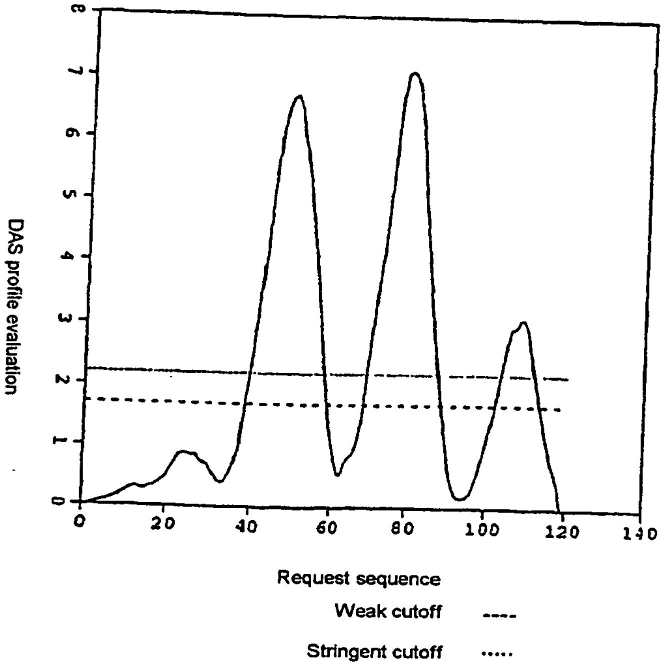
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Fig. 13

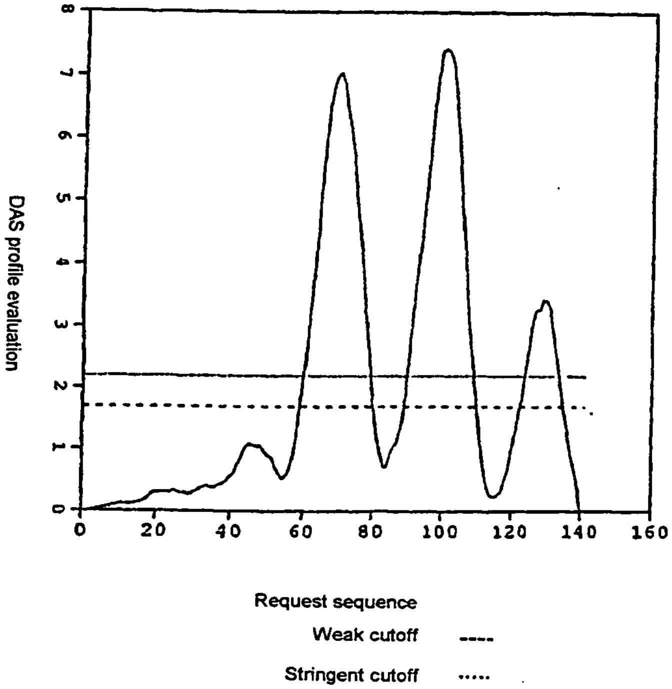
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Fig. 14

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Fig. 15

SEQ. ID. No. 14

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Fig. 16

SEQ. ID. No. 15

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Fig. 17

SEQ. ID. No. 16

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Fig. 18

SEQ. ID. No. 17

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Fig. 19

SEQ. ID. No. 18

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Fig. 20 Part 1

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CTGGCGTCTTCTAGGACACTTGTATCTGATCTTTACTGAAAGTCACATTCTTAGCAAGACTTAACCTTACATCCTGAGTA
AAATTGCGAATTCCACAGATGCCCTCAATCTTTCCTGACCTCGGCTCCTCTTCTGTTTCCCGGCATGGCTTGAAGCGCAA
CGGCATTCTACCTGTTTACTCAGGATGTGTCTTACCATTAAAGTCCCTGCCTGCAGAGCAGTTGGCTTGATTTCACCT

Fig. 20 Part 2

```
CHARACTERISTIC           Localization/designation
    mRNA                 Combine    (1..312,313..479,480..587,588..1437)
                          /Feature   ="CAT-A mRNA Exon 1-4 "
    Exon                 1..312
                          /Feature   ="CAT-A Exon 1"
    Exon                 313..479
                          /Feature   ="CAT-A Exon 2"
    Exon                 480..587
                          /Feature   ="CAT-A Exon 3"
    Exon                 588..1437
                          /Feature   ="CAT-A Exon 4"
    Div_Charakteristikum 275..703
                          /Feature   ="CAT-A ORF -Start-1"
                         /Translation="MGPHRLWMCLSACCPAVHAMPGIGPLAQTPVLW
                         RADLHRSGCVAAGAHCGIHFHRLETAPEQHSSLLQGPPVACSPLVSI
                         SAHVYLMMQMTTETWAQCGVWMLIGFAMYFGYGIPHSLENNQQPPAS
                         SSQTPHENIPSPLLN."
    Div_Charakteristikum 174..530
                          /Feature   ="CAT-A ORF-start-2"
                         /Translation="MNSVPKAESPACVPEASSTPASLWSPVSTIPTP
                         RWGRIVYGCAFLLVVLLSMLCLVLAHWPKRLFSGELIYIAAAVLLLV
                         LIVGFTFTVWRQPQSNTPLYFKVPLLPVLLWSASLHMFT"
                         Div_Charakteristikum    111..530
                         /Feature   ="CAT-A ORF-3"
                         /Translation="FRYQPDENFSKNEKPKEEVVEMNSVPKAESPAC
                         VPEASSTPASLWSPVSTIPTPRWGRIVYGCAFLLVVLLSMLCLVLAH
                         WPKRLFSGELIYIAAAVLLLVLIVGFTFTVWRQPQSNTPLYFKVPLL
                         PVLLWSASLHMFT"
    Div_Charakteristikum 482..667
                         /Feature   ="58%        homology to humans     -CAT3  GB
                         Acc. AF320612"
    Div_Charakteristikum 482..667
                         /Feature   ="63% Protein    homology to   cationic
                         amino acid transporter 3 [Rattus norvegicus] GB
                         Acc.BAA20133.1"
    Div_Charakteristikum 452..682
                         /Feature   ="protein     homology to    ecotropic
                         retrovirus receptor [Rattus norvegicus] GB Acc.
                         BAB83893"
    Div_Charakteristikum 24..500
                         /Feature   ="hom-rat-baa20133.1-31%"
    Div_Charakteristikum 24..500
                         /Feature   ="hom-mouse-cat3-AAB09593-60%"
    Div_Charakteristikum 482..667
                         /Feature   ="hom-mouse-cat3-AAB09593-40%"
    Div_Charakteristikum 500..682
                         /Feature   ="hom mouse-cat2-AAA37372-42%"
NUMBER OF BASES     333 a    345 c    341 g    415 t

TGGATATGGGTAGATGAAACCTCGGATACGTGGGAGCTACCGTGGGTGTATTAGGCTCTCTGATGTTGGATGAAC
AGGGACCTGGGTTAATCTTGCCCTACTCTCTCTAATTCAGGTACCAGCCAGACGAGAATTTCAGCAAGAACGAGA
AGCCGAAGGAGGAAGTAGTTGAGATGAATTCTGTACCCAAAGCAGAATCCCCAGCATGTGTTCCTGAAGCGTCCA
GCACTCCGGCGAGTCTGTGGAGCCCTGTCAGCACCATCCCCACCCCGAGATGGGGCCGCATCGTCTATGGATGTG
CCTTTCTGCTTGTTGTCCTGCTGTCCATGCTATGCCTGGTATTGGCCCATTGGCCCAAACGCCTGTTCTCTGGAG
AGCTGATCTACATCGCAGCGGCTGTGTTGCTGCTGGTGCTCATTGTGGGATTCACTTTCACCGTCTGGAGACAGC
CCCAGAGCAACACTCCTCTTTACTTCAAGGTCCCCCTGTTGCCTGTTCTCCTCTGGTCAGCATCTCTGCACATGT
TTACCTGATGATGCAGATGACCACTGAGACCTGGGCCCAATGTGGAGTCTGGATGTTGATTGGATTTGCTATGTA
TTTTGGATATGGGATCCCACACAGCTTGGAGAACAATCAACAGCCACCAGCGTCAAGCTCCCAAACTCCTCATGA
AAACATCCCTAGTCCCTTGCTGAATTAGTTTAACCACGGAAAAGGGATGGTCCAGTCCACTGGAGGTGTCCTCTG
GATGAAGGGAAAGTGTGAAGCTCTGTGGAGCATGAAGGTGGGATACACTTAAAGCCCCTTGTGCATTGCCAGTGA
GCAAACACTTTTTAAAAAACTTTATTTTGTTGTTTGTTTGTTTGTTTGTTTGTTTGTTTGTTATAGAGGTGAGGA
CTTGCTCTGTTGCCCAGGCGGAACTTGAACTCCTGGGCTCAAGTGATCCTCCTGCCTCAGTCTTCCAAGCAGCTG
GGACTACAGGTACCCCATCATACCCAGCTTAACAAAATATCTTTATTTGATTTGATTTTTTTTCTTTTTGAGACA
```

Fig. 21 Part 1

GAGTCTCGCTCTATTGCCCAGTCTGGAGTGCAGTGGCATGATCTTGGCTCACTGCAACCTCCGCCTCCCGGGTTC
AAGTGATTCCCCTGYGTGAGCCTCCAGAGTAGCTGGAATTACAGGCACATGACACTGTGCCCAGCTAATTTTTCT
TTATTAGYAGAGACCAGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCAAGTGATCCACCTGCC
TCGGCCTCCCAAAGTGCTGAGATTACAGGCCTGAGCCACCGTGCCCAGCCAAAATAACTTTAAAAACTTACATTT
TTAAAAATTGACAAAYAAAAGTTGTCTATGTTTATGGTGTACAATTGCATATATTATATGTATTAAAATTGTGTA
TGTTTATGGTAT

Fig. 21 Part 2

TTTTTTAATTAGTATTTATTTCTGTTCCTTTCATACATGTTATTGTTCAGGCAGCAGTCTTACATACCTATCTGA
AATAATCTACCATCACACACTCTAGTTAAAGCCAAAGCTCCGTAGGTAAAGCTGACCAGCTGTCCAGAGTTCTCA
GCTCATGGAATCTTGCTTCTTGATTTTATGTTAATTTCTGAAAGTCAGAAATGTCATCTCCAAAAAGTGTTAAGG
GGGTTGTAAAAAATAATCACTATATTTGCTATTATAGTTGTAGGTATGCAGTATATTTTCTTTTCTTTCTTTCTT
TCTTTTTTTTTTTTTGAAACAGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCAGCGATCTAGGCTCACT
GCAGCCTCCGCCTCCCAGGTTCACGTGATTCTCCTGCCTCAGCCTTCCAAGTAGCTGGGATTACAGGTGCCCCGC
CACCACCACGCCCGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCAACATGGTGGCCAGGCTGGTCTGGAA
CTCCTGACCTCGTGATCTGCCCACCTTGGCCTCCCAAAGTGCTGGGACTACAGAAGTGAGCCACCGCGCCTGGCT
TGTATTTTCTTAAAGAAATAAAAAACTAAGAAGAAAATGCCACTCATCATCATTGGTATAGCAATGTGGTCAGCA
GGAAAAGAAAATACTGTGATAAATTTGTCTCTTTAATAAAGAAGAAATTCTAGTCCAAGCTTCAATACACTTCCT
GGTTTTTCACTAGATATTTCTTTTACTGCTGCTCTTCCTTCTTTTCTACATCTCATATTAGAGGATTGGACAGCC
TTTAAAACTTCATTGACAGGAGCAAATCCAGTATGCACTGATTTCTTTTTTTTTTTTCTTTTTTTTTTTTTGGTG
AGACGGAGATTTACTCTTGTTGTCCAGGCTGGAGTGCAATGGTGCGATCTCGGCTCACCGCATCCTCTGCCTCCC
GGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGACATGTGTCACCACGCCTGGCTAAT
TTTGTATTTGTAGTAGGGATGGGGTTTTACCATGTTGCCCAGGCTGATCTCGAACTCCTGACCTCAGATAATCCG
CTCGCCTCGGCCTCCCAAAGTGCTGGGATTGACAGGCGTGAGCCACTGCACCCAGCCTGATTTCTTCTTAAAGGC
ACTCTAACCCATCAGAGAGCCCGGTAGTTTCATTCTCACGAATACTCTAGCCGTGAAAAAAACTCAATAGGACAC
AGACGAATCCAACGAATAGAAGAAGAAATCTATTGAGTTTTGGGATATTTGGTGCATTCGATCGGTCCAGGATTA
TGAAACCTAAACCTCCCATTGTAAACAGGAAGCTGGATCCAAGTCCTTCCATAATAATATTGTCCACTTACTCTG
TAGGCCAAGAAAGCTACTGGCCTCTGATGCCCTTGTTCATCAGTCATAGAGCCAACACCTGGCGGTTCAACCGTA
ACATCATAAACGATTCCTCTGGTGATGAGGAAGTAAGACACCACCACCAGAGCATACATAGTCATGGCCAACGGC
ATGTGCAGCCAGGGCGGCTTCTTCAGCTTCAGGTTGGGACATTCAAGCGCTAAGAACGGGACACGGTACAAAGTC
TCCATGTTGGTGGCAGCAAGGGCCATTCTCGGCCTC

Fig. 22

CHARACTERISTIC

	Localization/designation
Exon	1..288
Div_Charakeristikum	/Feature = "Exon 3" complementary (1..288) /Feature = " homologous to XM_034710-mRNA-782-1070 end section.seq(1>288)"
Exon	621..863
Div_Charakeristikum	/Feature = "exon 2" complementary (621..863) /Feature = " homologous to XM_034710-mRNA-539-782-part.seq(1>244)"
Exon	1183..1686
Div_Charakteristikum	/Feature = "Exon 1" complementary (1183..1686) /Feature = " homologous to XM_034710-mRNA-37-538-part.seq(1

NUMBER OF BASES 426 a 403 c 350 g 507 t

TTTTTTAATTAGTATTTATTTCTGTTCCTTTCATACATGTTATTGTTCAGGCAGCAGTCTTACATACCTATCTGA
AATAATCTACCATCACACACTCTAGTTAAAGCCAAAGCTCCGTAGGTAAAGCTGACCAGCTGTCCAGAGTTCTCA
GCTCATGGAATCTTGCTTCTTGATTTTATGTTAATTTCTGAAAGTCAGAAATGTCATCTCCAAAAAGTGTTAAGG
GGGTTGTAAAAAATAATCACTATATTTGCTATTATAGTTGTAGGTATGCAGTATATTTTCTTTTCTTTCTTTCTT
TCTTTTTTTTTTTTTTGAAACAGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCAGCGATCTAGGCTCACT
GCAGCCTCCGCCTCCCAGGTTCACGTGATTCTCCTGCCTCAGCCTTCCAAGTAGCTGGGATTACAGGTGCCCCGC
CACCACCACGCCCGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCAACATGGTGGCCAGGCTGGTCTGGAA
CTCCTGACCTCGTGATCTGCCCACCTTGGCCTCCCAAAGTGCTGGGACTACAGAAGTGAGCCACCGCGCCTGGCT
TGTATTTTCTTAAAGAAATAAAAAACTAAGAAGAAAATGCCACTCATCATCATTGGTATAGCAATGTGGTCAGCA
GGAAAAGAAAATACTGTGATAAATTTGTCTCTTTAATAAAGAAGAAATTCTAGTCCAAGCTTCAATACACTTCCT
GGTTTTTCACTAGATATTTCTTTTACTGCTGCTCTTCCTTCTTTTCTACATCTCATATTAGAGGATTGGACAGCC
TTTAAAACTTCATTGACAGGAGCAAATCCAGTATGCACTGATTTCTTTTTTTTTTTTCTTTTTTTTTTTTTTGGTG
AGACGGAGATTTACTCTTGTTGTCCAGGCTGGAGTGCAATGGTGCGATCTCGGCTCACCGCATCCTCTGCCTCCC
GGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGACATGTGTCACCACGCCTGGCTAAT
TTTGTATTTGTAGTAGGGATGGGGTTTACCATGTTGCCCAGGCTGATCTCGAACTCCTGACCTCAGATAATCCG
CTCGCCTCGGCCTCCCAAAGTGCTGGGATTGACAGGCGTGAGCCACTGCACCCAGCCTGATTTCTTCTTAAAGGC
ACTCTAACCCATCAGAGAGCCCGGTAGTTTCATTCTCACGAATACTCTAGCCGTGAAAAAAACTCAATAGGACAC
AGACGAATCCAACGAATAGAAGAAGAAATCTATTGAGTTTTGGGATATTTGGTGCATTCGATCGGTCCAGGATTA
TGAAACCTAAACCTCCCATTGTAAACAGGAAGCTGGATCCAAGTCCTTCCATAATAATATTGTCCACTTACTCTG
TAGGCCAAGAAAGCTACTGGCCTCTGATGCCCTTGTTCATCAGTCATAGAGCCAACACCTGGCGGTTCAACCGTA
ACATCATAAACGATTCCTCTGGTGATGAGGAAGTAAGACACCACCACCAGAGCATACATAGTCATGGCCAACGGC
ATGTGCAGCCAGGGCGGCTTCTTCAGCTTCAGGTTGGGACATTCAAGCGCTAAGAACGGGACACGGTACAAAGTC
TCCATGTTGGTGGCAGCAAGGGCCATTCTCGGCCTC

Fig. 23

CHARACTERISTIC	Localization/designation
Exon	748..1035 /Feature ="Exon 3"
Div_Charakteristikum	748..1035 /Feature =" homologous to XM_034710-mRNA-782-1070-end section. seq(1>288)"
Exon	505..747 /Feature ="Exon 2"
Div_Charakteristikum	505..747 /Feature =" homologous to XM_034710-mRNA-539-782-part .seq(1>244)"
Div_Charakteristikum	1..504 /Feature ="Exon 1"
Div_Charakteristikum	1..504 /Feature =" homologous to XM_034710-mRNA-37-538-part .seq(1>502)"

NUMBER OF BASES	307 a	194 c	222 g	312 t

```
GAGGCCGAGAATGGCCCTTGCTGCCACCAACATGGAGACTTTGTACCGTGTCCCGTTCTTAGCGCTTGAATGTCC
CAACCTGAAGCTGAAGAAGCCGCCCTGGCTGCACATGCCGTTGGCCATGACTATGTATGCTCTGGTGGTGGTGTC
TTACTTCCTCATCACCAGAGGAATCGTTTATGATGTTACGGTTGAACCGCCAGGTGTTGGCTCTATGACTGATGA
ACAAGGGCATCAGAGGCCAGTAGCTTTCTTGGCCTACAGAGTAAGTGGACAATATTATTATGGAAGGACTTGGAT
CCAGCTTCCTGTTTACAATGGGAGGTTTAGGTTTCATAATCCTGGACCGATCGAATGCACCAAATATCCCAAAAC
TCAATAGATTTCTTCTTCTATTCGTTGGATTCGTCTGTGTCCTATTGAGTTTTTTTCACGGCTAGAGTATTCGTG
AGAATGAAACTACCGGGCTCTCTGATGGGTTAGAGTGCCTTTAAGAAGAAATCAGTGCATACTGGATTTGCTCCT
GTCAATGAAGTTTTAAAGGCTGTCCAATCCTCTAATATGAGATGTAGAAAAGAAGGAAGAGCAGCAGTAAAAGAA
ATATCTAGTGAAAAACCAGGAAGTGTATTGAAGCTTGGACTAGAATTTCTTCTTTATTAAAGAGACAAATTTATC
ACAGTATTTTCTTTTCCTGCTGACCACATTGCTATACCAATGATGATGAGTGGCATTTTCTTCTTAGTTTTTAAA
GAAAATATACTGCATACCTACAACTATAATAGCAAATATAGTGATTATTTTTTACAACCCCCTTAACACTTTTTG
GAGATGACATTTCTGACTTTCAGAAATTAACATAAAATCAAGAAGCAAGATTCCATGAGCTGAGAACTCTGGACA
GCTGGTCAGCTTTACCTACGGAGCTTTGGCTTTAACTAGAGTGTGTGATGGTAGATTATTTCAGATAGGTATGTA
AGACTGCTGCCTGAACAATAACATGTATGAAAGGAACAGAAATAAATACTAATTAAAAAA
```

Fig. 24

CHARACTERISTIC	Localization/designation
Exon	2118..2524 /Feature ="Ex n 18"
Exon	1976..2117 /Feature ="Exon 17 "
Exon	1867..1975 /Feature ="Exon 16 "
Exon	1785..1866 /Feature ="Exon 15 "
Exon	1645..1784 /Feature ="Exon 14 "
Exon	1581..1644 /Feature ="Exon 13 "
Exon	1488..1580 /Feature ="Exon 12 "
Exon	1298..1487 /Feature ="Exon 11 "
Exon	1144..1297 /Feature ="Exon 10"
Exon	1113..1143 /Feature ="Exon 9"
Exon	1024..1112 /Feature ="Exon 8"
Exon	888..1023 /Feature ="Exon 7"
Exon	730..887 /Feature ="Exon 6"
Exon	597..729 /Feature ="Exon 5"
Exon	484..596 /Feature ="Exon 4"
Exon	400..483 /Feature ="Exon 3"
Exon	367..399 /Feature ="Exon 2"
Exon	1..366 /Feature ="Exon 1"

NUMBER OF BASES 475 a 814 c 729 g 506 t

```
GGCGCGCCCGGGGTGCCGCTCCCTGCCTGGCGCGCTCCGCACCTGGAGGTGCCTTGCCCCTCTCCTGCCCACCTC
GGAATTTCCCTGTGGCTCCTTTGATCCTTCGAGTCTCCAGCTCCTCTCCCTTCCACCTGTTTCCCCCAAGAAAGG
CAGGATCCTGGTCCCTGCTACGTTTCTGGGGCCATGGCTGGTCTGGGCCCCGGCGTAGGCGATTCAGAGGGGGGA
CCCCGGCCCCTGTTTTGCAGAAAGGGGGCCCTGAGGCAGAAGGTGGTCCACGAAGTCAAGAGCCACAAGTTCACC
GCTCGCTTCTTCAAGCAGCCCACCTTCTGCAGCCACTGCACCGACTTCATCTGGTGAGGGAAGGGGGCAGGGCCT
GCAATGTCAAGGTAAGAGCTGGGGTGGTTCATCGACGATGCCACGAATTTGTGACCTTCGAGTGTCCAGGCGCTG
GGAAGGGCCCCCAGACGGACGTGAGTGCTCGGACCGGAACAAACACAAGTTCCGCCTGCATAGCTACAGCAGCCC
CACCTTCTGCGACCACTGTGGCTCCCTCCTCTACGGGCTTGTGCACCAGGGCATGAAATGCTCCTGTGAGTGAGA
TGAACGTGCACCGGCGCTGTGTGCGTAGCGTGCCCTCCCTGTGCGGTGTGGACCACACCGAGCGCCGCGGGCGCC
TGCAGCTGGAGATCCGGGCTCCCACAGCAGATGAGATCCACGTAACTGGTGAGGGAGGCCCGTAACCTAATTCCT
ATGGACCCCAATGGTCTCTCTGATCCCTATGTGAAACTGAAGCTCATCCCAGACCCTCGGAACCTGACGAAACAG
AAGACCCGAACGGTGAAAGCCACGCTAAACCCTGTGTGGAATGAGACCTTTGTGTTGTGAGTCCTGAAGCCAGGG
GATGTGGAGCGCCGGCTCAGCGTGGAGGTGTGGGACTGGGACCGGACCTCCCGCAACGACTTCATGGGGGCCATG
TCCTTTGGCGTCTCGGAGCTGCTCAAGGCGCCCGTGGATGGCTGGTGACAAGTTACTGAACCAGGAGGAGGGCGA
GTATTACAATGTGCCGGTGGCCGATGCTGACAACTGCAGCCTCCTCCAGAAGTTTGAGGTACTGTAACTACCCCC
TGGAATTGTATGAGGTGAGCGGGTGCGGATGGGCCCCTCTTCCTCTCCCATCCCCTCCCCTTCCCCTAGTCCCAC
CGACCCCAAGCGCTGCTTCTTCGGGGCGAGTCCAGGACGCCTGCACATCTCCGACTTCAGCTTCCTCATGGTTCT
AGGAAAAAGGCAGTTTTGGGAAGGGTGATGCTGGCCGAGCGCAGGGGCTCTGATGAGCTCTACGCCATCAAGATCT
TGAAAAAGGACGTGATCGTCCAGGACGACGATGTGGACTGCACGCTGGTGGAGAAACGTGTGCTGGCGCTGGGGG
GCCGGGGTCCTGGCGGCCGGCCCCACTTCCTCACCCAGCTCCACTCCACCTTCCAGACCCCGGACCGCCTGTATT
TCGTGATGGAGTACGTCACCGGGGGAGACTTGATGTACCACATTCAACAGCTGGGCAAGTTTAAGGAGCCCCATG
CAGCGGTTCTACGCGGCAGAAATCGCTATCGGCCTCTTCTTCCTTCACAATCAGGGCATCATCTACAGGGGACCT
GAAGCTGGACAATGTGATGCTGGATGCTGAGGGACACATCAAGATCACTGACTTTGGCATGTGTAAGGAGAACGT
CTTCCCCGGGACGACAACCCGCACCTTCTGCGGGACCCCGGACTACATAGCCCCGGAGGATCATTGCCTACCAGC
```

Fig. 25 Part 1

CCTATGGGAAGTCTGTCGATTGGTGGTCCTTTGGAGTTCTGCTGTATGAGATGTTGGCAGGACAGGCCTCCCTTC
GATGGGGAGGACGAGGAGGAGCTGTTTCAGGCCATCATGGAACAAACTGTCACCTACCCCAAGTCGCTTTCCCGG
GAAGCCGTGGCCATCTGCAAGGGGGGTTCCTGACCAAGCACCCAGGGAAGCGCCTGGGCTCAGGGCCTGATGGGG
AACCTACCATCCGTGCACATGGCTTTTTCCGCTGGATTGACTGGGAGCGGCTGGAACGATTGGAGATCCCGCCTC
CTTTCAGACCCCGCCCGGTGTGGCCGCAGCGGCGAGAACTTTGACAAGTTCTTCACGCGGGCGGCGCCAGCGCTG
ACCCCTCCAGACCGCCTAGTCCTGGCCAGCATCGACCAGGCCGATTTCCAGGGCTTCACCTACGTGAACCCCGAC
TTCGTGCACCCGGATGCCCGCAGCCCCACCAGCCCAGTGCCTGTGCCCGTCATGTAATCTCACCCGCCGCCACTA
GGTGTCCCCAACGTCCCCTCCGCCGTGCCGGCGGCAGCCCCACTTCACCCCCAACTTCACCACCCCCTGTCCCAT
TCTAGATCCTGCACCCCAGCATTCCAGCTCTGCCCCCGCGGGTTCTAGACGCCCCTCCCAAGCGTTCCTGGCCTT
CTGAACTCCATACAGCCTCTACAGCCGTCCCGCGTTCAAGACTTGAGCG

Fig. 25 Part 2

CHARACTERISTIC	Localization/designation
Source	complementary (1..24801) /Organismus="Homo sapiens" /db_xref="taxon:9606" /Chromosome="19" /Clone="CTC-331H23"
Exon	24395..24801 /Feature ="Exon 18 "
Exon	24005..24146 /Feature ="Exon 17"
Exon	22324..22432 /Feature ="Exon 16"
Exon	20762..20843 /Feature ="Exon 15"
Exon	18300..18439 /Feature ="Exon 14"
Exon	18108..18171 /Feature ="Exon 13"
Exon	17922..18014 /Feature ="Exon 12"
Exon	16128..16317 /Feature ="Exon 11"
Exon	15647..15800 /Feature ="Exon 10"
Exon	11054..11084 /Feature ="Exon 9"
Exon	10680..10768 /Feature ="Exon 8"
Exon	10201..10336 /Feature ="Exon 7"
Exon	9368..9525 /Feature ="Exon 6"
Exon	7580..7712 /Feature ="Exon 5"
Exon	7332..7444 /Feature ="Exon 4"
Exon	1862..1945 /Feature ="Exon 3 "
Exon	864..896 /Feature ="Exon 2"
Exon	1..366 /Feature ="Exon 1"

NUMBER OF BASES 5613 a 6407 c 6621 g 6160 t

```
GGCGCGCCCGGGGTGCCGCTCCCTGCCTGGCGCGCTCCGCACCTGGAGGTGCCTTGCCCCTCTCCTGCCCACCTC
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CAGGATCCTGGTCCCTGCTACGTTTCTGGGGCCATGGCTGGTCTGGGCCCCGGCGTAGGCGATTCAGAGGGGGGA
CCCCGGCCCCTGTTTTGCAGAAAGGGGGCCCTGAGGCAGAAGGTGGTCCACGAAGTCAAGAGCCACAAGTTCACC
GCTCGCTTCTTCAAGCAGCCCACCTTCTGCAGCCACTGCACCGACTTCATCTGGTGAGGGAAGGGGGCTGGGGGA
CTGGGGGACGAGGGGACTAGGGGTGCAGACTCCTATCACGCCGACCCCTGTGGAAGGAAGAAGGAGGGGGCTGTA
GTCCCGACTCCCAGGTTCTAGGATGGCCAGGGAACGCTGGGAGCTTCGACTCCTGGGTTTCAGTGAGGAGGAGGC
TGGTTCCTGGAGTGCTGGGTCCGAGGGAGGAGGAGGCTGGAGGACAGAGGTCCTGGAGTCTTGGGTCTGAGGGAG
GAAGGGCCTGGGGGGCTGGGAGCCTGGATTCCTGGGTCTGAAGGAGGAAGAAACTGGGGGCTGAACTCCAGTCTA
AGGGAAGAAGGGCTGGGGGCCAAAATTTCTGGGTTCTAGAAAGAGGAGGTGGCCGGGGCTTGGACACCTGGGCCC
TGCGGGAGGAGGGTCAGAGAGCGCAGGCCCCCTGTGGCTCGCAGAGGTTGGGGGTCCAGGTACCCCTTTCTGCAC
TGACCTAGGATCCCTGACTCTTCCAGGGGTATCGGAAAGCAGGGCCTGCAATGTCAAGGTAAGAGCTGGGGACCG
GGGCTCCTGGGACCCTCAGGAGGGTGGAGGCTGGGGCCCCACAGCTGAGGCTGCTTGACACACGTGTTCTCTGGT
CCCCAGAGAGGCGCGGGGGAGCCCGGGGCGGGGGGTGTGGCAGAGACACAGCCTGTGGTGGGGAGGGAGCTTTGA
TGGTGGGGCCACCGCGGAGGTGGTGCTGGGGGCCCCTCCCTCGGCCGGCTCCAGGTGGGGACAGATATTTGGAGA
ATCTGTTGCCATGGGAACATGGAGATTTGGAAAAGGGGAGCTGAAGGGGGGAAGGGGGAGGGGGCTGGAGATGCA
AAGTCAGAGCCCCCCCCCACCCCAGGCTGCCGTCGCCATGACAACACCAGCCGTCCTAGGCAGGGGCAGGCCGGG
```

Fig. 26 Part 1

```
TGGGGTCACCAATGGGCGAGTGGGGGCCGGGCGGGGCCGGCAGTTCTGGGGGGCGGGAGAGGGGGGCGAGTCCTT
GAGCACCAGCTGCTACTGCTGAGAACAGAGTGAGTCAGGGTGGGGGGCGGGCCGGCAGCAGCGCCCCCAGACTCA
CTTCTGCCCAAGTTGCTGCTTCCTGGGCTGCGTCTGAAGATATTTCGGTTTTCGCTCTTTGAATCTGTCTGCCTC
TCTCCTGGCTTTCTGATCTCCGTCCGTGGGCCTGTGTCTGTTTGTCAATGGGATCCTATTTTCTTTCTCTCTTTT
TCCATCTCCCTTCCCTGAGCTCTGTGCTCTGTGTCTCTCTGTAAGTCTCTGCGTCTCTGTTTCTGACTCTGAGCC
CATCTCTTGGGTTTCTGTCTCCTGCTTCTCTCTCTGGCCTCCGATTTTCTCTCTGTTGGACTCTCTGTGTTGAGA
TCCCTCTCTTTCTGGTTTTCTCAGTGTCCGAGTTCCGCTCTCTCTTTCCAATTTTCTGTCTGCTGGGGTCTCCCG
CTGGACTAATCCATGCCTCCGTCTGTGTCTCTATGATTTTCATCTATAGTCTGCAGCTTTGTGGTTCATCGACGA
TGCCACGAATTTGTGACCTTCGAGTGTCCAGGCGCTGGGAAGGGCCCCCAGACGGACGTGAGTGCTCGGACACCT
GGTTCTCCTCCTCGGGCCGTGCCCCCGCCCTCACCCCCTCGGCGTCCGTCCCAATTTCTCCTGCTATTTTTATGG
CTGGGAGGGGAGGGGGGCTGGAGAGATAGGGGGAGCTATCTGGCCCAGATTCCTTGCCCTTGGCCTGGAAAGGGG
GAATGCGAGGGGGACTGACAGGCTGGGGACACGGGTGGGGCACAGAGAGGAGGCCGGGGTGAGGAGACTGAAGAT
GGGTGCTGCCGGGGGTGGGCTGTGATCCAGGGGTGAAGGGATTTAAAAATTGAGAGCTGAGGGGCACACGGAGAA
AAATATCAGTGCAGGTGCGGAGATGCCAACATAAGACAGAGGGAATCTCAGGGAGAGGAACAGAGACAGAAGAAG
ACAGAGACCTAGGAGAGACTGAAGCTGAGGCAGAGAGAGAGAGAGATGGAGCAGAGAAAGAACCAGGGAGAAAGA
GAGGAATTTGGAGGCACCAAAAGATGGACAGAGAAACTCCAAGAGACGGAGACACAGACACCTGGAGAAAGAGAC
TAAAATAGAAAATGGTGGATACAGACAACAGCTTAGGAGATGCTGAGAGGAGACCCAGGGAAGTCCCACAGTACA
CTTGCACACATGTGCGTGCATGTACAGATGCCCCTGTCATCACAGATGTGCAGCACGCAGAGACACACAGCCTCT
CCCCACCCCCTCTCTCTCCATCAGAGGCTCACAAGACCAGTCAACCCTGAGTGCCCATTCCCGTTCCCTTTTCTG
CTTTATCTCTGAGCCTCAGTTTCCTCCTCTATAAAATGGGGCTGATGATCTAGCATTGACCAACAGAACTGTTTA
CAGTGACGGAAGCATTCTGTACATGCACTGTCCAATAGGCAGCCACCAGCTCCATGTAGCCAGTGAGCACTTGAA
ACAGGGCGACTGTGGCTGAGGATTAGAAATTCCATTTCGTGTCATTTGAATTGGCTTAAATTTTTTTTTTTTATT
TTTATTTTTTGAGACGGAGTCGCGCTCTGTTGCCCAAGCTGGAGTGCAGTGGCGCAGTCTCAGCTCAATGCAACT
TCCGTTTCCCAGGTTCAAGCAATTCTTCTACCTCAGCCTCCTGAGTAGCTGGGACTACAGGCGCATGCCACCACA
CCCCGCTAATTTTTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGA
CCTTGTGATCCACCCGCCTCGGCCTCCCAAAGTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGGCAGAACTGA
CTTAAATTTAAACAGCCACATGTAGTTAGTGGCCACCAAATGGGACAGCACACATCTGGACACTTCCAGGCTTGT
TTTGAAGTCAGGTGGGTTCAGAGTTTCGCCCAGGGTTTGACACAAGATCGGAGACAGTTTTATGATGTACAGATG
GAGAGAGAGGCAGAGAGAGAGAGATCCACAGAAGTCCATGAGGCGTTTTACCACCCTCTCAGCTGAAAATAACAG
AAGTCTACATAGAAGATGTGACTTCATAGAACATATATTGAGCACCACTGTCTACCAGCACGTGTATGTGATTGA
TGACCCCCCTCGTCCACTCACCTCCGCCACCAACACCAGATAAGTCTGATGCATCCAGTGCTCATTGGGTACACT
CATCAAGATTTTTTTTTTTGTTTTTTGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGAATTGCTTGAACCT
GAGCGGCAGAGGTTGCAGTGAGCCAAGATCACGCCACTGCACTCCAGCCTGGGTGACAGAGCAAGACTTTGTCTT
GGAAAAAAAAAAAAAGATTTTTTTTTGTTTTTGTTGTTTTGTTTGATTTTGGGGTATTTTTTAGATGGAGTTTCA
CTCTGTCACCCAGGCTGGAGTGCACTGGTGCAATCTTGGTTCACTGCAACCTCTACCTCCCAGGTTCAAGCGATT
CTCATGCCTCAGCCTCCCGAGTAGCTGGGACTAGAACAGGCATGAGCCACCATGGCCGGCTAATTTTTATATTTT
TAGTAGACAGGGTTTCATCATGCTGGCCAAGCTGGTCTTGCTCCTGACCTCACGTGATCCACCCACCTCGGCCTC
CCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCACCCAGCCGATTTTTGGGGTTTTTTGAGACAGGGTCCCACT
CTGTCACCTAGACTGGAGTACAGTGATGGGATCATAGCTCACTGCAGCCTTGAATTCTCCAGGCTCAAGTGCTCC
TCCTGCCCCAGCTTCTCAAGTAGCTGGGACTATAGGCACAAGCCACAACACCTAGCTAATTAAAAAAAAATGTTT
TTGTAGAGATGGAGTCTCACTCACTATATTGCCCAGGCTGGTCTTCAACTCCTGGTCTCACTCGATTCTCCTGCC
TCAGCCTCCCAAAATGATGGGATTACAGGCGTGAGCCACTGCACCTGGCCTCAAGTATTTTGTATACAGTATAGG
TTGGATCCACACAACAGCTTATTTGGTTATTTTTCCCTGTCTATCTGGTTTGAATCCCAGCTCCACCACTTTTTG
GTTCTGTGACATTTCCTGAGTTAATTTACCTCTCTGCACTTGTTGAATTCCTTGTTTGTAAAGTGGAGATGATAA
TTATGCTCACTATGGATTGTTTTGAAGATTTAGTGAGTCAGACATTTGGGATGGTTTCTGACACATAGCAAGAGC
CAAAATATTATTTTTTATTCTTGTTAAAATTATTATTATGACCAATGAGGAAACGAGTGAATAGTGAGAAGGAGA
TCTTTCCTCTGCATCACTCGGGGGTTTTTTTGTTTTTGTTTTTTTTTGCTGTTGAGACAGGGTCTCACTCTGTTG
CCCAGGCTGGAGTGCAATAGTGCTATCACTGCTCACTGCAGTCTTGACCTCCGGGGCTCAAGTGATTCACTGCTG
GCAGTTGATCTTCTTAAAAGTAACATGCAGGCCAGGCACAGTGGCTCACGCCTGTAATCCCAACACTTTGGGAGA
CCGAGGCGGGTGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACATGGAGAAGCCACGTGTCTACTA
AGAATACAAAATTAGCTGGGCGTGGTGGCACACGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATC
ACTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCAAGATTGCGCCATTGCACTCCAGCCTGGGCAGCAAGAACAA
AACTCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGTAACATGCCTTGACCAGGCATGGT
GGCTCATGCCTGTAATCCCAGCTCTTTGGGAGGCTGAGGCAAGCGGATCACGAGGTCAGGAGATCCAAACCATCC
TGGCTAACGCGGTGAAACCCCGTCTCTACTAAAAATACAAAAAATTAGCCAGGCACGGTGGCACGCGCCTGTAGT
CCCAGCTACTCGGGAGGCTGAGGCAGGAGTATCGCTTGAACCCGGAGGCAGAGGTTGCAGTGAGCCGAGATCAC
ACCACTGCACTCTAGCCTGGGCGACAGAGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAAAAGTAACATGGAT
CAAGATTTGGCAAGAATGATTTCATTTAGTCCCCAGGGAGGGCACATGCCCCCACTTTTCAAGCGGTAAATCTGA
GGCTTTGAAAAGGGGCAGGCGTGGTGAGGCCACCTAGCTGGGTAGGGGATAGAGGCAAGATTTGAACTCTGATGT
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TCTGTGGATGGTTTGTGTGTCAGGCAGCCTGCTGAGAACCTTCACACACAGCATCTTATTTAGTGCGGCAGGAAC
CCTTTGAGTTAGGGTCAGCGGAGATATTTAGAAGCCCAGCACATTGAAAAGGATCCTGGAAACTGCCAACACCCT
CCTCTACCCAAATATATATTCAAACTAGAAACCCCACTAACATAGATGAAAATCCAAGAATGGCCTAAATGTTCA
```

Fig. 26 Part 2

CCCTGTGATAATCCTTTTAATGGATTCTTAGAATCAAGTTATTTAACAAGCAGATATTGTCCCGGGGGTAGTGGG
TGGCAGGGGAGAAGGAGAAGCTTCACTGATGACCTGCATTCTTGCTTAATGGACTCTGGAAATTTAGCATTGCTT
CAAAATATAGATTATTTATTTCCACTTGACAGAGGAGGATGCTGAGGCTCAAAACTGGGAATGAACTTGCCCCAA
ATCACACAGCTGAGAAGCGGCCTAGCTCTTACTTACATTCAGGGCTATGTAGGGACTTCAATAAAATCCCTAACA
ATAACCACAGTAATAGTATTGGGAGCATCTAACGTGGTAGGCACAGCTATGTTTTGTACACCAATTATTTTATTT
AGGCCTCCTGGGTTCCTATTATAACTGAGAGGTCATGTTCTCCATTCCACCTGGAGCTCAGAGAAGGCATACCAT
ATGGACACTGACAGAAGCTGCCAGTGAAGGAGCTGGGGTTCAGGGTGGCCCACAAGTCCTCAAATAATAACTTGT
GGGAGTTGGGGGATGGGAACTATGGGAGGTTGGAAGCTCCTGCCTCCTTCATGTTCTGCCCAGATATCATTTGG
TCAGCGAGGCCCCCCTGCCACTCCCCCTGCACACAGTTTTGTTGTTGTTGTTGTTTGAGACAGAATCTTGCT
CTGTCATCCAGGCTGGAGTGCAGTGGCACAATCTTGGCTCACTGCAACCTCGGCCTCCTGGATTCAAGCAATTCT
CATGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCATGCACCACCATGTCCGGCTAATTTTTGTATTTTTAGTA
GAGACAGAGTTTTGCCATGTTGCCTAGCCTGGTCCGGAACTCCTGAGCTCAAGGCAATCCGCCCACCTCGGCCTC
CCAAAGTGCTGGGATTACAGGCATGAGCCACCGCACCCAGCCAGGACCACCGTATTTAAAATTTCAATCCCCCAA
CTTCTGGTGGTCCCCATCCCTGCCTCATTTTTTCTCCAGAGCACCCATTACCAACCATCAAACTATATGTTTTAT
TTATTTACCATGTTTACATTCTGTATCCCTCCATTAGGAAGTAAACTCCATGTGACAAAGAGGTTTTTTTTTTTC
ATTTGTTTAATGCTGGGTCCCCACACCAAGAACAGTCCCTGGCACACAGCAGGTGCTCAATGATTATTGGTACAT
AGAGTGAAAGAGATGGAGCCTCAGGCTGACCTAGAGAGCAAGGCAGGAGGAAAAGATAAAAGGGCCCCTCCCCTG
GGGTTTTAGGACCCTCCCAACGCCCCCTAAGCCAGTCTTCTCTGCCCCCAGGACCCCCGGAACAAACACAAGTTC
CGCCTGCATAGCTACAGCAGCCCCACCTTCTGCGACCACTGTGGCTCCCTCCTCTACGGGCTTGTGCACCAGGGC
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CCGGGATGGGGTGGGGGGTGGAGTCTTGGCTTGGGGGCGGGGCCTGAGGTGCTACCCGCAGCTTTCCCCTCCAGG
CTGCGAGATGAACGTGCACCGGCGCTGTGTGCGTAGCGTGCCCTCCCTGTGCGGTGTGGACCACACCGAGCGCCG
CGGGCGCCTGCAGCTGGAGATCCGGGCTCCCACAGCAGATGAGATCCACGTAACTGGTGAGGCCCCGCCCCCTCG
CCTGGCCCCGCCCCCTCCCCAAGTGTGAGGCGGGGCTGACCCAAGGCACTTGTGCTGGCCCAGCCCTACCCCAAA
GATGGGGCCACGCCTCTTTCTATGGTCACGCCCACACTCCTGACCCCACCCCAAAGGCCGAGCACACCCAGCCAT
ACCCCTTTTGGCTCGAAGCCCCGCCTCCAACCTGGCTTCTTGCAACTTTCTGCACCTGTTAATGACTTTGACTTT
CTTTTTTTTTTTGGGACGGAGTTTCGCTCTTGTTGCTCAAGCTGGAGTGCAATGGCGCGATCTCGGCTCACTGCA
ACTTCCGCCTCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCGCGTGTCACC
AAGCCCGGCTAATTTTTTGTATTTTTAGTACAAACGGGGTTTCACCATGTTAGCCAGGCTGGTCTCGAACTCCTG
ACCCCAGGTGATCCCCTCGACTCGGCCTCCCAAAGTGCTGGGATTAACAGGCGTGAGCCACCGCGCCTGGCCAAT
GGCTTTCTTTTTTGTTTTTATTTTATGTTTATTTTTTTGAGATGGAGTCTTGCTCTGTCACCCAGGCTGGAGTGC
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TGTTGCCCAGGCTGGAGTGCAGTAGCATGATCTCAGCTCACTGCAACCTCCGCCTCTCAGGTTCAAGCGATTCTC
CTGCTTCAGCCTCCTGAGTAGCTGGGACTACAGGTGCATGACACTGCACCCAGCTCATTTTTGTATTTTTAGTAG
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CCGCCTCAGCCTCCTGAGTAGCTGGGACCACAGACACCTGCCACCACGCCCAGCTAATTTTTTTTTTTTTTTGTA
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CCTGACGAAACAGAAGACCCGAACGGTGAAAGCCACGCTAAACCCTGTGTGGAATGAGACCTTTGTGTTGTGAGT
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TGGGAGGGGTTAGGATAGAGGGAACCCAGAAAAGGGCAGAAGAAGATGGTGGGAAAAGGGAATAGAGTGATTGAG
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GAGAGGAGAGAAGGGTACAGAGACTCAGAGAGAGAGATCTCGAGAGACAAGAGACAGAGATGGGAAGGGGCGGAG
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AGCACCAAGGATGGGGAACCGAGGGGAGCCATGAGCTCGGCTCTGCACCCCATCCACCCCACCTTCCTGCAGCAA
CCTGAAGCCAGGGGATGTGGAGCGCCGGCTCAGCGTGGAGGTGTGGGACTGGGACCGGACCTCCCGCAACGACTT
CATGGGGGCCATGTCCTTTGGCGTCTCGGAGCTGCTCAAGGCGCCCGTGGATGGCTGGTGAGGAGCAGGGCTGGG
GCCTGGGGATGGAGCGCAATATTACCATCTCCATCTGTGTGTGGTCTCTCTCCTCCAGGCCACTGTCCTTCCCTC
TGCCTCCCAGCATGCGCACACACACACACACACACACACACACACGCACACACACGCACACACCCCTCTCTCTCT
ATTCTTCTCTTCTTCTCCCCTCCCTTTCTCCCTCTCCCTCTCTTTTTATCTCACTCTTTCTCTCTTCCATCTCTG
TGTCCGTCTCTCTGTGTCTCTTTCCTCCCTTCCAATGTCTTTGCCTCTCCCATGGGTGCCCCATCCCCGCTGCCC
GCCTCTGGTCTCCGTCTGTATGTCAGGTACAAGTTACTGAACCAGGAGGAGGGCGAGTATTACAATGTGCCGGTG

Fig. 26 Part 3

GCCGATGCTGACAACTGCAGCCTCCTCCAGAAGTTTGAGGTACCCAGACCCTGGCTTCCTCAAGGGAGCCCAGCC
CAGCCTCCCACGGTTCAGAGCTGGCCTTTCCTTCCACCCCTGAGTGCCCGCTGGTCCTGGGACTACAGTTCCCAG
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CTATCGCCATGGCTTGAGGGTACTAGGGGCCACCAGCCCCTGTTCTAGGGCGATCCCCTGCATCTCTTGGGACCC
TGACTCTCTCTTTCTTTTCTCCCAGGCTTGTAACTACCCCCTGGAATTGTATGAGGTGAGTAGAACCAGGGCGTT
GAATGGAGGCAGTTTTTGCCTACTTCTCTGATTTCTTATTCCTCCTCTGACTTCTGTCTTCAATTCCCCACACAT
GAGTTGAGCACACATTTGTGCTAGGCCTGTCTTGTGCTTGCTGAATAATCCAGGATCCAGAGATGAATCTGACCC
TCAAGCAACTCTCCAAGGTAGGGACACAGTCACAGATACTTAAAATACAGGAAGATGTGCTAAATTAGAGGTAGC
CCAGGGCACTGAAGAGGCCTAACGGAGGCACTAATCCAGCCTGGGGGAGGGTGGTCAGGGAGGACTTCCCTGAGG
AGGTGACGCCTGAATTGATTCTTGAGGTTTTTTAAAATTTTTTAATTTATTTTTATTTTTATTTTTATTTTTATT
TCTGTCGCCCAGGCTGGAGTGCAATGGCACAATCTCGCCTCACTGCAACCTCCAGCTCCCGGGTTCAAGCAATTC
TCTTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGTGACCGCCACCACACCCAGCTAATTTTTTTTTTATTTTT
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CTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCGACCGATTCTTGAGTTTTTTATTTTTTTTTTGAG
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GCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACACCCAGCCGATTCTTGAGTTTTAAAAAATC
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ATACTTTACAGAGCATCTTTGTGTGCCAGGCGTGGCTCTACTCACTGGGGATATAGAGAAAGCAGGGAAAGAACA
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ACCCAGCCCTCAACAAATATTTATGTAGCCTCAATGAGGTAGGCAGTGTTACTGTGTCTTAGCGAACAAAGCAGA
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CCAGGAAGGTGCTGTCCATGGTGACCAAGGGGTGGTAAGAGAGGCATCTGACCCAGTTTAAAAAGTCAGGCGAGG
CCTCTATGAAGTGATGCTTGAGTCAAGGTCTAAAGGGTGTTTGGGAGACAACTAGGAGGGAAGGGGAGGGGAGAG
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GCTGGACCATGGAGCCTGGGAGAGAGAAGAACAACCTGCAGTGTCAGTCTCAGCCTGGCTCTGCAAGTCATGTGG
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AGCTGAAAGCCAGGTGTGCTCCCTGGACTGGCAGCACCCATGTCACCCAGAAGCTTTTTACACATAACGATTCTC
AGGTCCCACCCCAGATTTATAGAGTTAGAAAATCTGGCAGTGGACCCAGCAATCTGTTTTACCAAACCCTCTAG
GGAATTCCGGCTTAGAGGCTAAGAGCAACCAGATTCTAGAGCTGGACTGCTTGGGTTTCATTTCTGGCTCTGTCC
TTTACCTGCTGTGTGACTTGGGGCAAGTTACTTAACGTCTCTGTGCTAGTCTCCTCTTCTGTAAAATGGAAACGA
TAGCAGGGTTTTCTGGAAACAGCATATGATAAGCTATCTAAAAAAAAAAAAGAAGAAAAAAAGAGCTAAGTGTTT

Fig. 26 Part 4

GTTGAATAATAAATAAACCCTCCAGGCTATGGGGAGTCAGAGAAAATTAAGCCAAGGACAGGGTAGGAGGGTGGC
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TGTGTAAGGTCTAACTGCCTCTGGCTCTTTCTTTCTCCTTTCCACAGCGGGTGCGGATGGCCCCTCTTCCTCTC
CCATCCCCTCCCCTTCCCCTAGTCCCACCGACCCCAAGCGCTGCTTCTTCGGGGCGAGTCCAGGACGCCTGCACA
TCTCCGACTTCAGCTTCCTCATGGTTCTAGGAAAAGGCAGTTTTGGGAAGGTTGGATTCCTGGGGTTCTGGGGA
AAGGGAGGATGTCTGTGGGAAGGTCAGATTTCTGGTTCTTAGGGAGGAAGTGGGGGTGGGAAGAGACTGGGCTCC
TGCATCTTCAAATATGGTTAGGTTGGGCCGTTCAGGTTCCTGGAGAGGAGAGGTTTACAGATGTGGACACTCTCC
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GCGTCCCTTAGGGAGGGGGCAGGTCCTGTACCACTGGGTTCCCAACATGGACTGGCCCTTTTGGAACTGTGCGCA
TAGGTGATGCTGGCCGAGCGCAGGGGCTCTGATGAGCTCTACGCCATCAAGATCTTGAAAAAGGACGTGATCGTC
CAGGACGACGATGTGGACTGCACGCTGGTGGAGAAACGTGTGCTGGCGCTGGGGGGCCGGGGTCCTGGCGGCCGG
CCCCACTTCCTCACCCAGCTCCACTCCACCTTCCAGACCCCGGTAAGGATGGAGGGGGCGGAGGCTGTCCTCCGG
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GAGTAGCTGGGATTACAGGCTCCCGCCACCACACTCAGCTGATTTTTGTATTTTTAGTAGAGACCGGGTTTCGCC
ACGTTGGCCAGGCTGGTCTGGAACTCCTGACCTCAGGTGATCCACCCGCTTCGGCCTCCCAAAGTGCTGGGATTA
CAGGCGTGAGCCACCACGCCCAGCTGCAACTTTGATTCTTAGTAGGAAGCCAGAATTGCATCTGTGTGTGAGTGG
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CTTCTGACGTCCCCACCCACCCCGTCCTCCAGGTTCTACGCGGCAGAAATCGCTATCGGCCTCTTCTTCCTTCAC
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AACGTCTTCCCCGGGACGACAACCCGCACCTTCTGCGGGACCCCGGACTACATAGCCCCGGAGGTAACCCCAACC
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GACCCTCAGACCTTGTCATGAGTTGTGGCCTTCTTACACAGCCAGTCGTTCCTCCAGCCTCCAGCACAGGTGAGC
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CCAGCCTGGGTGACAGAGCATAACTTCATAACTTCATCTCAAAAAAAAAAAAAAAAAAAAAGCCGGGTGCAGTGGC
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TGCACTCCAGTCTGGGCAACAGAGTGAGACCCTGTCTCAAAAAAAAAAAAAAAAAAGAAAAAGAAAAAGGGCAGGG
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GCAGATCACTTGAGGTCAGGAATTCAAGACCAGCCTAGCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAA
AAATTAGCTGGACATGGTGATGTGTGCCTGTCAACCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAAC
CCAGGAGGTGGAGGTTGCAGTGAGCCAAGATTGCACCACTGCACTGCATCCTGGGCTACAGAGTGAGACTCCATC
TCAAAAAAGAAAAAAGATAAGAAAATTTGAAAACTACACACATATTCCTGACTCTGACACAAATATTCTAGGTGG

Fig. 26 Part 5

GTGGAACCAGTGACTTGGCCGTTAGGTAGTCTTTCTATTTGAGGCCAAATGAATGTTTGAAGTAGGTATGCTTTG
TTTCCAGAATATTCCAAAAGTTAGATCGCTGGCCAAAATATTCAGAGTGGAGGCTGGGCGTGGTGGCTCACTCCT
ATAATCCCAGCACTTTGGGAGGCGGAGGCAGGCCAATTGCTTGAGTCCGGGAGTTTGAGACCAGCCTGGGCAACA
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GGGAGGCTGAGGTAGAAGAATTACCTGAGCCTGGGAAGTTGAGGCTGAGTGAGCCGTGATCACACTACTGTGCTC
CAGCCTGGGCAACAGAGTGAGACCCTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAACGAAACAAAAAATCACCTGA
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CAGAGGGGTCCTAGGCTTCCTAAAGAACGCATCATGATTCCCTGCCTTCCACCTCCCCTAGATCATTGCCTACCA
GCCCTATGGGAAGTCTGTCGATTGGTGGTCCTTTGGAGTTCTGCTGTATGAGATGTTGGCAGGACAGGTAAGGGA
AGGTGGGGAGAAGCTGGCTTGGCTAAAAGAGACAGAGAGGGGCACCTGGATCTCAGGAGGAGCCAGTTAGAAAGG
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GGACTGCTGAGTGTACTACAACTAAAAAAATTGGTTACCACACTCTTGATCATCTTCTTAGCTGGCTATGGTAGT
GGGCACCTATAGTCCCAGCTACTGGGGAGGCTGAGGCAGGAGGGTCACATGAGCCCAAGAACTCAAGGTTACACT
GAACTATGAGTATGCCACTGTGTTCCAGCACAGGCGACAGAGCAAGACCCCATCTCAAAAGAACAAACAAACAAA
AGAAATCAATCATTTTGAAAGATAGTCACCAAAACTTTTAAAATTTAATTGAATCTAACAACCAACTAAATTCAA
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CAACCAGGAGAATGCTTTTAGGGTGTTTCCTGCAGTTTTTCCTCTCTTCTATTTAACTGACATGTTGCATAATTA
ACAGCCTGCTGATTTACATAGCAGATAAAGAGAGGCAGAATAGTACAGAGATGCACAGATCTGAGGCATCCGAGA
TAGGAAATGAGAGAACCTGAGAAGGAGAGAGATCAAGCTTTGGTGGTTTGGTCTGATCTCTCCTGAGGGTGTGGT
CAGGTGTGCATGTGGGGCGTGTGATGGGTCAGGCATGTTCCCGGTGGGGTGAGGAGGGTGTGGAAGGTTTGGGGA
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GAGCTGTTTCAGGCCATCATGGAACAAACTGTCACCTACCCCAAGTCGCTTTCCCGGGAAGCCGTGGCCATCTGC
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ACTCCCCAGCTCCCTGCTTGCAGGAAGTGCTGAAAGTCCAGGGTGTCTGTCTGTCTAGAACTGGGTGGGTCAGGT
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CTGCTGGCTTTCTGTCCTCCCTTTTCTCTGGGTCTCTGTCCCCATATTTGGTCTTTATTCCTCCCTCTGGGTGTG
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CTGTCCTTCACTCTCCCCTTCCCTCCCTCCCCCTACCCTTCCCTCTCCCCGTCCCTCTCTCCCCTTCCCTCTCTC
CCCCTACCCCTTTTCCCTCTCCTCTTCTCCATCTCCCTCATGATTTGTTCTGTTTCTCTGTGTGTCCCTGGGTCT
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TCACTCTCACCCTCTGTCTCTCTCTCTCTCTGTCCCTCTTCCTCTCTCTCTCCTCTCTGTCTCTCTCTGTCTCGC
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TCTGCAGGAGACAGGAGATGAGACTGGGGTACACAGAGGGACACCCGAGGAGCCCTCGGAGCTGCTTAACTTTCC
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Fig. 26 Part 6